Genetic profile for Entiat NFH

Summer Chinook salmon

3-14-2012

Prepared by

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National Fish Hatchery Broodstock Genetic Profile

Facility: Entiat National Fish Hatchery

Stock: summer Chinook salmon (*Oncorhynchus tshawytscha*)

Parental stock: Mixture of adipose-clipped and unmarked adults collected at Well's Hatchery

Year founded: 2009

Generation time: 3 years (10%), 4 years (86%) or 5 years (4%) [Ref 1]

Segregation / Integration history: Segregated. The program is not intended to establish or support any wild-spawning population, but rather to provide harvest opportunities.

Table 1 - Broodstock samples analyzed:

Description	Year	n	Life stage	Data source
Entiat NFH broodstock	2009	88	returning adult	AFTC
Entiat NFH broodstock	2010	99	returning adult	AFTC

Table 2 – Summer Chinook salmon samples analyzed for comparison:

Description*	H/W	Year	n	Life stage	Data source**
Eastbank Hat. (M)	H	1992	33	returning adult	WDFW
Eastbank Hat. (M)	H	1993	86	returning adult	WDFW
Eastbank Hat. (M)	H	2008	88	returning adult	WDFW
Eastbank Hat. (W)	H	2008	90	returning adult	WDFW
Methow River	H	2008	18	returning adult	WDFW
Methow River	H	2009	18	returning adult	WDFW
Methow River	W	2006	90	returning adult	WDFW
Methow River	W	2008	87	returning adult	WDFW
Methow River	H	2009	80	returning adult	WDFW
Okanogan River	H	2006	49	returning adult	WDFW
Okanogan River	H	2008	18	returning adult	WDFW
Okanogan River	H	2009	107	returning adult	WDFW
Okanogan River	W	2006	88	returning adult	WDFW
Okanogan River	W	2008	92	returning adult	WDFW
Okanogan River	W	2009	126	returning adult	WDFW
Wells Hat.	H	1991	42	returning adult	WDFW
Wells Hat.	H	2006	91	returning adult	WDFW
Wells Hat.	H	2008	91	returning adult	WDFW
Wenatchee River	H	2006	70	returning adult	WDFW
Wenatchee River	H	2008	83	returning adult	WDFW
Wenatchee River	W	1993	133	returning adult	WDFW
Wenatchee River	W	2006	168	returning adult	WDFW
Wenatchee River	W	2008	168	returning adult	WDFW

*Eastbank Hatchery stocks represented include Methow (M) and Wenatchee (W)

**WDFW data published in Kassler et. al [Ref 2]

Genetic markers analyzed:

GAPS microsatellites [ref 3] (13 / 13 loci). A complete list of the markers analyzed is provided in Appendix 1. Genotyping success rates are presented in Appendix 2.

Table 3 - Diversity within samples. Expected (H_e) and observed (H_o) heterozygosity, allelic richness rank (AR rank, with 1 representing the most diversity and 13 representing the least diversity), number of loci exhibiting departures from Hardy-Weinberg Equilibrium (HWE), F_{IS} (a measure of departure from random mating), number of pairs of loci exhibiting linkage disequilibrium (LD), and effective population size (N_e) based on LD are listed for each sample. Samples in which we observed no evidence for any disequilibrium caused by genetic drift due to a finite number of parents (i.e. those with an estimated N_e of infinity) have N_e marked by "-".

No	Description	H_e	H_o	AR rank	HWE	F_{IS}	LD	N_e
1	Entiat NFH broodstock 2009	0.87	0.87	2	2	0.00	8	790 (322 - Infinite)
2	Entiat NFH broodstock 2010	0.86	0.86	25	3	-0.01	31	166 (123 - 244)
3	Eastbank Hat. (M) 1992	0.86	0.86	3	1	0.01	2	-
4	Eastbank Hat. (M) 1993	0.86	0.86	10	1	0.00	2	18,696 (383 - Infinite)
5	Eastbank Hat. (M) 2008	0.86	0.86	18	0	-0.01	0	-
6	Eastbank Hat. (W) 2008	0.85	0.85	7	2	0.02	3	-
7	Methow River H 2008	0.84	0.84	8	0	-0.02	1	788 (74 - Infinite)
8	Methow River H 2009	0.85	0.86	17	0	-0.03	12	70 (32 - Infinite)
9	Methow River W 2006	0.86	0.86	13	4	0.02	4	2,184 (355 - Infinite)
10	Methow River W 2008	0.86	0.86	4	1	-0.01	2	1,272 (281 - Infinite)
11	Methow River H 2009	0.85	0.85	22	2	0.00	0	-
12	Okanogan River H 2006	0.86	0.86	5	3	-0.02	21	97 (63 - 186)
13	Okanogan River H 2008	0.85	0.85	12	2	0.02	1	148 (47 - Infinite)
14	Okanogan River H 2009	0.85	0.85	20	4	-0.01	34	-
15	Okanogan River W 2006	0.86	0.86	1	3	0.00	41	232 (151 - 454)
16	Okanogan River W 2008	0.86	0.86	16	2	-0.01	4	-
17	Okanogan River W 2009	0.86	0.86	11	0	0.01	1	-
18	Wells Hat. 1991	0.86	0.86	24	0	0.00	3	102 (65 - 216)
19	Wells Hat. 2006	0.87	0.87	14	2	0.00	20	-
20	Wells Hat. 2008	0.86	0.86	6	2	0.00	13	332 (185 - 1,161)
21	Wenatchee River H 2006	0.85	0.85	18	2	0.03	16	135 (88 - 255)
22	Wenatchee River H 2008	0.86	0.86	9	4	0.01	20	171 (114 - 313)
23	Wenatchee River W 1993	0.85	0.85	21	0	-0.01	10	1,066 (379 - Infinite)
24	Wenatchee River W 2006	0.85	0.85	23	1	0.00	3	-
25	Wenatchee River W 2008	0.85	0.85	14	3	0.01	20	1,440 (498 - Infinite)

Figure 1 - Correspondence Analysis (CA) of allele frequencies observed in Entiat NFH broodstock and adjacent summer Chinook salmon populations. Sample numbers are those listed in Table 3. Axis 1 and 2 accounted for 8.5% and 7.6% of the variance, respectively.
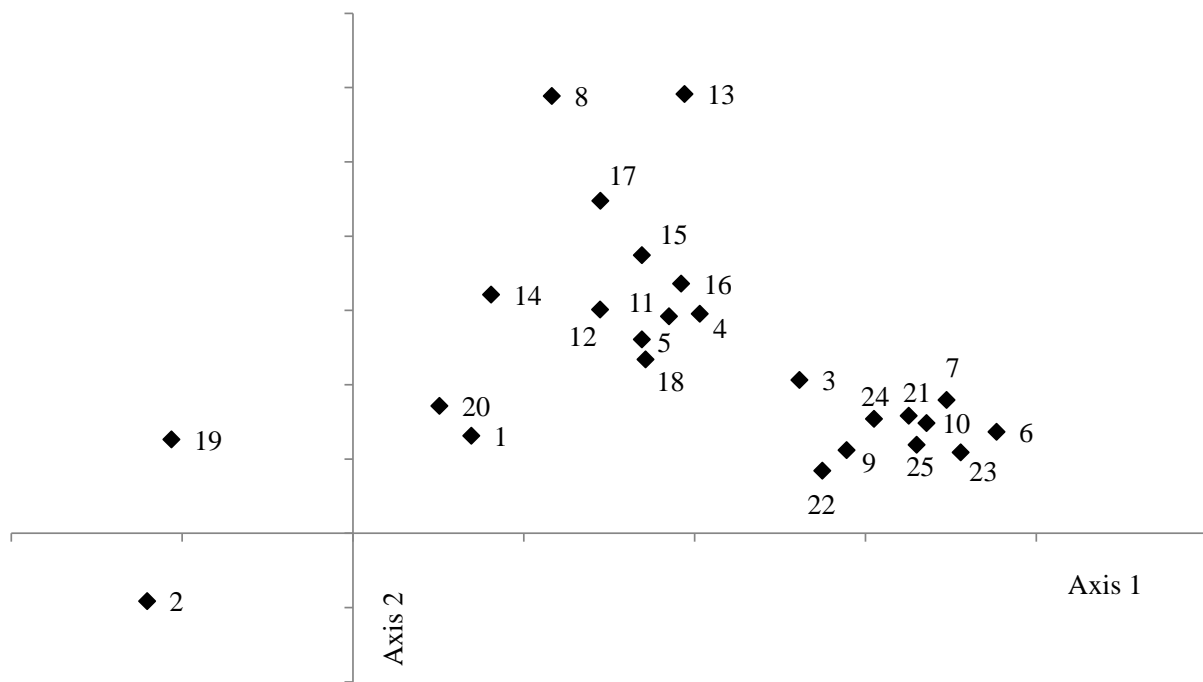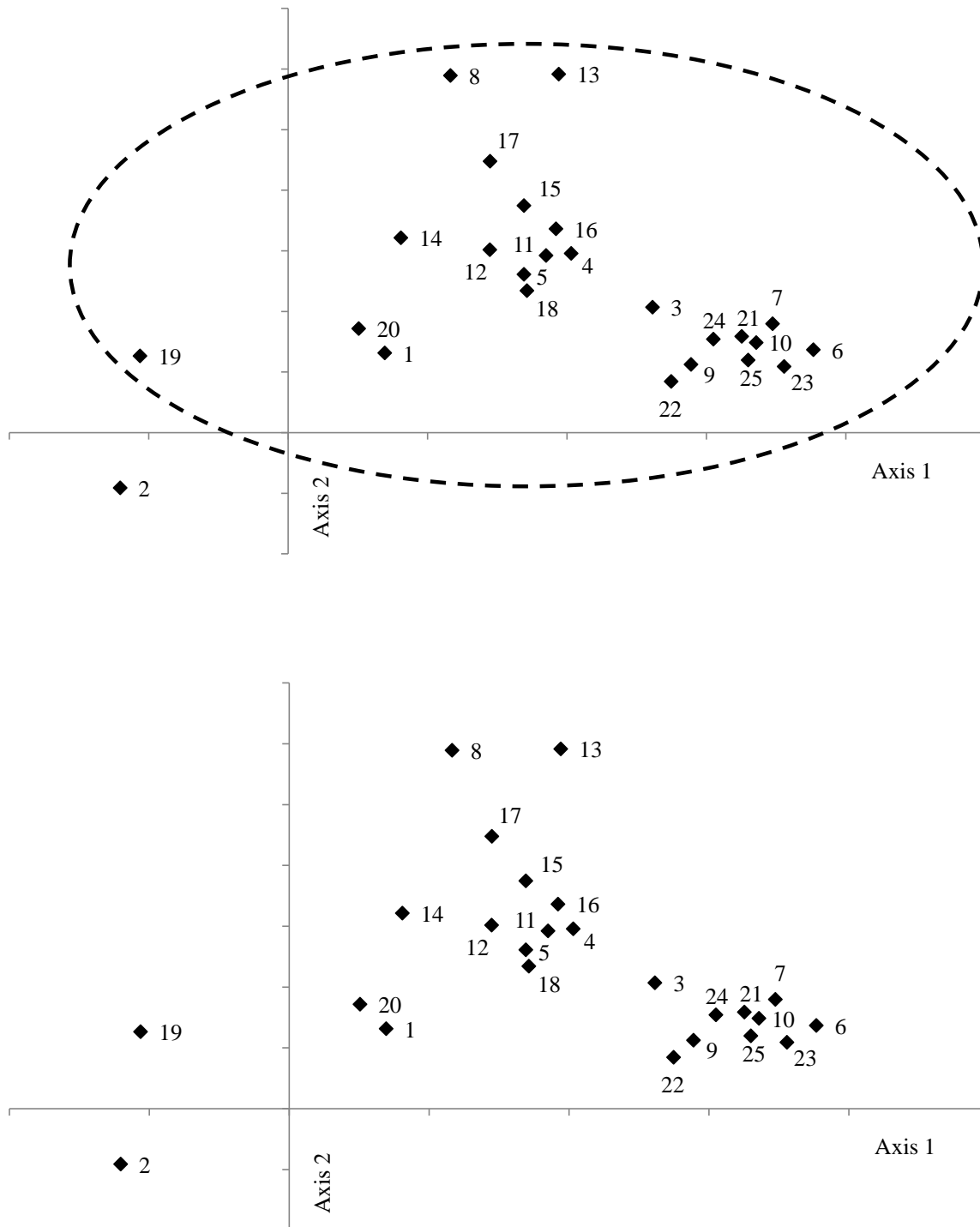
Figure 2 - Statistical tests of divergence among samples from Entiat NFH and adjacent summer Chinook salmon populations. Sample numbers are those listed in Table 3. Dashed lines indicate groups of samples lacking statistically different allele frequencies (top) and statistically significant F_{ST} values (bottom).

Comments

- The goals of this report series are 1) to summarize available genetic information for NFH broodstocks and make that information available to hatchery managers, and 2) to make sure that data for the NFH broodstocks are available for internal hatchery reviews and HET meetings, as well as to our partners.

- Correspondence Analysis did not reveal any clear pattern of genetic structure among the collections. The two most divergent collections, separated from the others along the x-axis, were the Entiat NFH 2010 broodstock and the Wells Hatchery 2006 broodstock.

- Only the Entiat NFH 2010 broodstock exhibited significantly different allele frequencies from all other collections. F_{ST} between Entiat NFH 2010 and Wells Hatchery 2006 was not significant (Figure 2; Appendix 3).

- The above result is concordant with prior genetic analyses of upper Columbia River fall and summer Chinook salmon which have revealed broad genetic similarity within the ESU. This homogeneity is thought to be the result of confinements, translocations and culture activities performed to mitigate for the construction of Grand Coulee Dam.

- Entiat NFH broodstock were among the most diverse and least diverse samples based on Allelic Richness (AR; Table 3), however, estimates of average AR are quite similar for all of these collections (range 12.1 to 12.9)[Ref 4], so the pattern is probably not meaningful.

- The Entiat 2010 broodstock exhibited a higher LD and HWE and lower Ne than the 2009 broodstock (Table 3). These results may reflect family or population structure among the samples collected at Wells Hatchery in 2010. Possible explanations include that a few families were disproportionately represented in this collection, or that the collection includes individuals from multiple populations.

Sources cited

1. Based on 2008 brood year at Wells Hatchery, as reported in:

Snow C, Frady C, Repp A, Murdoch A, Small MP, Bell S, Dean C. 2011. Monitoring and evaluation of Wells and Methow hatchery programs in 2010. WDFW Report Available: http://www.fishlib.org/library/Documents/StreamNet_References/WAsn17094.pdf

2. Information regarding the microsatellite markers used and the inter-agency baseline in which they are used may be found in the following article:

 Seeb LW, Antonovich A, Banks MA, Beacham TD, Bellinger MR, Campbell M, Garza JC, Guthrie CM III, Moran P, Narum SR, Stephenson JJ, Supernault KJ, Teel DJ, Templin WD, Wenburg JK, Young SF, Smith CT. 2007. Development of a Standardized DNA Database for Chinook salmon. Fisheries 32: 540 - 552.

3. Kassler TW, Blankenship S, Murdoch AR. 2011. Genetic Structure of upper Columbia River Summer Chinook and Evaluation of the Effects of Supplementation Programs. Washington Department of Fish and Wildlife Final Report: 33 pp.

4. Smith CT, Adams B. 2011. Summer Chinook salmon in the Entiat River: genetic analysis of hatchery and natural origin adults spawning in the wild. AFTC Report: 24pp.

Availability

Genotype data and allele frequencies for NFH stocks are available from Abernathy Fish Technology Center upon request.

Disclaimer

Appendix 1. Thirteen microsatellite markers used to analyze Entiat NFH summer Chinook salmon.

Microsatellite Markers	
1	Ogo2
2	Ogo4
3	Oki100
4	Omm1080
5	Ots201b
6	Ots208b
7	Ots211
8	Ots212
9	Ots213
10	Ots3M
11	Ots9
12	OtsG474
13	Ssa408

Appendix 2. Genotype call rates (completeness of data). Shaded cells indicate data that are <90% complete.

Description	Year	Microsatellite call rate
Entiat NFH broodstock	2009	0.997
Entiat NFH broodstock	2010	0.998
Eastbank Hatchery (M) H	1992	0.993
Eastbank Hatchery (M) H	1993	0.950
Eastbank Hatchery (M) H	2008	0.941
Eastbank Hatchery (W) H	2008	0.960
Methow River H	2008	0.944
Methow River H	2009	0.893
Methow River W	2006	0.976
Methow River W	2008	0.976
Methow River H	2009	0.887
Okanogan River H	2006	0.956
Okanogan River H	2008	0.936
Okanogan River H	2009	0.899
Okanogan River W	2006	0.972
Okanogan River W	2008	0.978
Okanogan River W	2009	0.919
Wells Hatchery H	1991	0.940
Wells Hatchery H	2006	0.909
Wells Hatchery H	2008	0.995
Wenatchee River H	2006	0.952
Wenatchee River H	2008	0.955
Wenatchee River W	1993	0.968
Wenatchee River W	2006	0.969
Wenatchee River W	2008	0.956

Appendix 3. Pairwise F_{ST} values between collections of summer Chinook salmon. Sample numbers are those listed in Table 3. Shaded cells indicate non-significant results (pairwise F_{ST} values not >95% of a null distribution in which individuals were permuted among samples).

	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
1	0.001	0.000	0.001	0.002	0.004	0.004	0.004	0.001	0.001	0.002	0.002	0.004	0.002	0.001	0.002	0.002	0.003	0.000	0.001	0.001	0.002	0.003	0.002	0.002
2	-	0.003	0.004	0.003	0.007	0.007	0.008	0.003	0.003	0.003	0.005	0.010	0.003	0.003	0.004	0.004	0.004	0.001	0.003	0.004	0.003	0.004	0.004	0.004
3		-	-0.001	-0.002	-0.002	0.006	0.002	-0.001	-0.001	-0.001	-0.002	0.000	0.000	0.000	-0.001	0.000	-0.001	0.000	-0.001	0.000	-0.002	0.000	-0.001	-0.001
4			-	0.001	0.002	0.008	0.002	0.001	0.000	0.000	0.000	0.000	0.002	0.001	0.000	0.000	0.001	0.002	0.000	0.002	0.002	0.001	0.001	0.001
5				-	0.003	0.007	0.005	0.001	0.000	0.002	0.001	0.003	0.001	0.002	0.001	0.002	0.001	0.002	0.002	0.002	0.001	0.002	0.002	0.002
6					-	0.005	0.003	0.001	0.000	0.000	0.004	0.000	0.004	0.002	0.002	0.003	0.003	0.006	0.002	0.002	0.001	0.001	0.000	0.001
7						-	0.012	0.005	0.003	0.002	0.005	0.012	0.007	0.004	0.004	0.005	0.009	0.009	0.007	0.002	0.005	0.005	0.004	0.005
8							-	0.001	0.004	0.004	0.005	-0.004	0.010	-0.001	0.005	0.002	0.004	0.003	0.002	0.004	0.005	0.003	0.006	0.005
9								-	-0.001	0.000	0.003	0.003	0.002	0.000	0.002	0.001	0.001	0.002	0.000	0.000	0.001	0.000	0.000	0.000
10									-	-0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.000	0.000	0.000	-0.001	0.000	-0.001
11										-	0.002	0.001	0.002	-0.001	0.001	0.000	0.003	0.002	0.001	0.001	0.000	-0.001	0.000	0.000
12											-	0.005	0.003	0.003	0.003	0.002	0.003	0.003	0.002	0.004	0.003	0.003	0.004	0.004
13												-	0.006	0.001	0.001	0.003	0.005	0.007	0.000	0.006	0.003	0.003	0.003	0.003
14													-	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.002	0.002	0.002
15														-	0.001	0.000	0.003	0.003	0.000	0.002	0.001	0.002	0.001	0.001
16															-	0.001	0.004	0.002	0.002	0.003	0.001	0.002	0.001	0.002
17																-	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002
18																	-	0.002	0.001	0.002	0.003	0.004	0.002	0.003
19																		-	0.001	0.004	0.003	0.004	0.004	0.004
20																			-	0.002	0.002	0.002	0.002	0.001
21																				-	0.002	0.001	0.001	0.001
22																					-	0.001	0.000	0.000
23																						-	0.000	0.000
24																							-	0.000

Appendix 4. Glossary

Allele – A unique genetic character state. Each locus has two alleles.

Allelic richness – The number of alleles observed in a sample of individuals, corrected for unequal sample sizes by rarefaction.

Effective population size (N_e) – The number of individuals in a model population which would lose genetic variation at the same rate as an observed population. Deviations from model behavior in real populations (e.g. unequal sex ratios, some individuals reproducing more than others, etc…) tend to make N_e lower than census size (N).

F_{IS} – Correlation of alleles in an individual relative to the subpopulation in which it occurs. Commonly used as a measure of departure from random mating within a subpopulation.

F_{ST} – Correlation of alleles within the same subpopulation relative to the entire population. Commonly used as a measure of divergence between subpopulations.

Gene flow – Movement of genetic material from one population to another. Implies both physical movement and successful integration into the recipient population.

Genetic Drift – Process of genetic divergence between populations based on random sampling of alleles each generation.

Heterozygosity – Proportion of individuals in a population that are heterozygotes (i.e. do not have two identical alleles at a locus).

Hardy-Weinberg Equilibrium (HWE) – Genotype ratios expected under a random mating model.

Linkage Disequilibrium (LD) – A measure of departure from independence of alleles in a pair of loci.

Locus – A physical location on the DNA of an organism. The term "locus" is often used synonymously with "marker" or with any type of marker (e.g., "SNP" or "microsatellite").